FIG. 1

BLASTP - alignment of 359_protein (SEQ ID NO:2) against swiss | Q05017 | PHLX_RABIT PHOSPHOLIPASE ADRAB-B PRECURSOR (EC 3.1.-.-).//:trembl | Z12841 | OCPPHLIP_1

product: "Phospholipase"; O.cuniculus mRNA for phospholipase.

//:gp|Z12841|1690 product: "Phospholipase"; O.cuniculus mRNA for phospholipase.

This hit is scoring at : 0.0 (expectation value)

Alignment length (overlap): 1217

Identities: 77 %

Scoring matrix: BLOSUM62 (used to infer consensus pattern)

Database searched: nrdb

Q: 1 EAWNSLLASSRYSEQESFTVVFQPFFYETTPSLHSEDPRLQDSTTLAWHLWNRMMEPAGE EAW:SLLASS:Y:.QESF.VVFQPFFYE:: S. .:P LQD.TTLA .LWNRMMEP.G.

H: 259 EAWDSLLASSKYNTQESFAVVFQPFFYESSLSALLAEPPLQDPTTLALSLWNRMMEPIGR

KDEPLSVKHGRPMKCPSQESPYLFSYRNSNYLTRLQKPQDKLGEKSIFLISLCVSFQVRE K:EP.S K.:P::CP:QESPYLF:YRNS..LTR:.:PQ.KL :VRE KEEPFSEKERKPLRCPTQESPYLFTYRNSGQLTRVSQPQGKL----EVRE

prosite signature

GAEIRCPDKDPSDTVPTSVHRLKPADINVI**GALGDSLTAGN**GAGSTPGNVLDVLTQYRGL G.EIRCPDKDPSD:VPTSVHRLKPADI.VIGA:GDSLTAGNGAGS.PGN:LDVLTQYRGL GTEIRCPDKDPSDSVPTSVHRLKPADIKVIGAMGDSLTAGNGAGSQPGNILDVLTQYRGL

SWSVGGDENIGTVTTLANILREFNPSLKGFSVGTGKETSPNAFLNQAVAGGRAEDLPVQA SWSVGGD:NI.TVTTLANILREFNPSL:GFSVGTG:ET:..AF.NQAVAG.RA:.L QA SWSVGGDQNISTVTTLANILREFNPSLQGFSVGTGRETTSQAFFNQAVAGARADGLIPQA

RRLVDLMKNDTRIHFQEDWKIITLFIGGNDLCDFCNDLVHYSPQNFTDNIGKALDILHAE :RLV LMKNDTRI:FQEDWKIIT:FIGGNDLCDFCND V.YSPQNFTDNIG.ALDILHAE QRLVALMKNDTRINFQEDWKIITVFIGGNDLCDFCNDPVRYSPQNFTDNIGTALDILHAE

VPRAFVNLVTVLEIVNLRELYQEKKVYCPRMILRSLCPCVLKFDDNSTELATLIEFNKKF :PRAFVNLV.VLEI .LRELYQE.KV CPRMILRSLCPCVLKFDDNSTE:A:LIE K:: IPRAFVNLVKVLEISKLRELYQETKVSCPRMILRSLCPCVLKFDDNSTEIASLIETIKEY

QEKTHQLIESGRYDTREDFTVVVQPFFENVDMPKTSEGLPDNSFFAPDCFHFSSKSHSRA QE:T.QLI:SGRYDTR:DFTVV:QPFFE.V:MPKT.:GLPDNSFFAPDCFHFSSK:H:.A QERTQQLIDSGRYDTRDDFTVVLQPFFEKVNMPKTQDGLPDNSFFAPDCFHFSSKAHAHA

prosite signature

RAPSALHPTSVHALRPADIQV**VAALGDSLTAG**NGIGSKPDDLPDVTTQYRGLSYSAGGDG R:PSA PTSVHALRPADIQVVAALGDSLTAG GIGSKP:DL.D TTQYRGLSYS:GGDG RSPSASPPTSVHALRPADIQVVAALGDSLTAGIGIGSKPNDLSDGTTQYRGLSYSSGGDG

DDHRVNFHEDWKVITVLIGGSDLCDYCTDSNLYSAANFVHHLRNALDVLHREVPRVLVNL DDHRVNF.EDWKVITV IG.SDLCDYCTDSNLYSAANF..HLR:ALD.LHREVPR.LVNL DDHRVNFQEDWKVITVQIGASDLCDYCTDSNLYSAANFYDHLRDALDALHREVPRALVNL

VDFLNPTIMRQVFLGNPDKCPVQQASVLCNCVLTLRENSQELARLEAFSRAYRSSMRELV VDF:NP::.RQVFLGNPDKCPVQQAS.LCNCVL: RENS.ELARLEA.::AY:SS:RELV VDFMNPSVTRQVFLGNPDKCPVQQASALCNCVLSPRENSYELARLEALAQAYQSSLRELV

GSGRYDTQEDFSVVLQPFFQNIQLPVLADGLPDTSFFAPDCIHPNQKFHSQLARALWTNM SGRYDT:EDFSVVLQPFF.:IQLPVL.DG DTSFFAPDC:HPNQKFHSQL:RALW.NM ESGRYDTREDFSVVLQPFFHSIQLPVLQDGRLDTSFFAPDCVHPNQKFHSQLSRALWRNM

LEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCTEWKAS LEPLG.KT:.LDL.A:::TCPTQNEPFLRT RNS:YTYP :PA:ENWGSDFLCT.W.AS LEPLGGKTDALDLTAAITLTCPTQNEPFLRTFRNSDYTYPSRPAVENWGSDFLCTAWNAS

NSVPTSVHQLRPADIKVVAALGDSLTVSMGARPNNSSDLPTSWRGLSWSIGGDGNLETHT ..VP.SVH:L:P.DIKVVAALGDSLT::MGARP:NSSD P. WRGLSWSIGGDG LETHT RGVPNSVHELQPGDIKVVAALGDSLTLAMGARPSNSSDPPMFWRGLSWSIGGDGALETHT

TLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPDINLEK TLPNILKKFNP:LGFST.T EGT.GLNVA.:GARA:DMPAQA DLVERM:NSP:I:LEK TLPNILKKFNPSILGFSTGTLEGTMGLNVAVQGARAQDMPAQARDLVERMRNSPEIDLEK

DWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVMELASL DWKLVTLF:G NDLCH:CENPE... EYVQHIQQALD:L EELPR.FVNVVEVMELA.L DWKLVTLFVGGNDLCHFCENPEGSSEGEYVQHIQQALDVLYEELPRTFVNVVEVMELAGL

YQGQGGKCA-MLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQREDFA:Q.QGG:CA:LAAQ::CTC.::SQSS:E.QELKKVNWNLQ.G:S..SY HQY.QREDFAHQDQGGRCATLLAAQSHCTCFKYSQSSVEMQELKKVNWNLQSGLSRLSYSHQYVQREDFA

VVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRKTTSNN VVVQPFFQNTL.PLN RGDTDLTFFS:DCFHFS:RGHAEMAIALWNNMLEPVG.KTTSNN VVVQPFFQNTLVPLNGRGDTDLTFFSDDCFHFSERGHAEMAIALWNNMLEPVGHKTTSNN

FTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGIIGTVVW FT:SR.KLKCPSP:SPYLYTLRNSRLLPDQAE. P.VLYWAVPVAAG.GL::GI:..V. FTYSRTKLKCPSPDSPYLYTLRNSRLLPDQAEADPTVLYWAVPVAAGAGLLIGILAMVAG

RCRRGGRREDPPMSLRT 1216

R .R REDPP:SL.T

RGMRCRPREDPPLSLST 1456

Ser is the active site.

Transmembrane segment:

From 1176 to 1198: length= 23,

1176 VLYWAVPVAA GVGLVVGIIG TVV

FIG. 2.
Prosite search result

Access#	From->To	Name	Doc#
PS00016	1096->1099	RGD	PDOC00016
PS01098	150->161	LIPASE_GDSL_SER	PDOC00842
PS01098	502->513	LIPASE_GDSL_SER	PDOC00842

FIG. 3.

HMMPFAM - alignment of 359_protein (SEQ ID NO:3) against pfam|hmm|Lipase_GDSL Lipase/Acylhydrolase with GDSL-like m

This hit is scoring at: 168.6 Expect: 1e-46 Scoring matrix: BLOSUM62 (used to infer consensus pattern)

Q: 149 VIGALGDSLTAGNGAGSTPGNVLDVLTQYRGLSWSVGGDENIGTVTTLANILREFNPSLK : ALGDSLT G.G GS...: D ..QYRGLS S GD N... T.L.:IL.:

H: 1 kvvalGDSLtdgggngsestklkdnyrqyrglspssvgdgnfsngtvlpdilakalgikl

RIHFQEDWKIITLFIGGNDLCDFCND 277
R . Q:D .::T: :GGNDLCD: .D

rkksqkdpdlvtielGgNDlcdyfrd 146

FIG. 4.

HMMPFAM - alignment of 359_protein (SEQ ID NO:2) against pfam|hmm|Lipase_GDSL Lipase/Acylhydrolase with GDSL-like m

This hit is scoring at : 172.2 Expect: 8.7e-48

Scoring matrix: BLOSUM62 (used to infer consensus pattern)

Q: 501 VVAALGDSLTAGNGIGSKPDDLPDVTTQYRGLSYSAGGDGSLENVTTLPNILREFNRNLT V.ALGDSLT G.G GS:...L.D .QYRGLS S: GDG:..N T.LP:IL.: .

H: 1 kvvalGDSLtdgggngsestklkdnyrqyrglspssvgdgnfsngtvlpdilakalgikl

G------KMKDDH G :.VG. ..N.: LN AV GA.AEDL:.:..L: KM ... gVgikeksilfrvgklqengsltglNfAvgGataedllkrlpnlldqvikksqykmygks

RVNFHEDWKVITVLIGGSDLCDYCTD 629
R . .:D .::T: :GG:DLCDY .D

rkksqkdpdlvtielGgNDlcdyfrd 146

FIG. 5

HMMPFAM - alignment of 359_protein (SEQ ID NO:2) against pfam|hmm|Lipase_GDSL Lipase/Acylhydrolase with GDSL-like m

This hit is scoring at: 155.2 Expect: 1.1e-42 Scoring matrix: BLOSUM62 (used to infer consensus pattern)

Q: 857 VVAALGDSLTVSMGARPNN--SSDLPTSWRGLSWSIGGDGNLETHTTLPNILKKFNPYLL V.ALGDSLT . G ..: .D ..:RGLS S GDGN... T.LP:IL.K . L H: 1 kvvalGDSLtdgggngsestklkdnyrqyrglspssvgdgnfsngtvlpdilakalgikl

DINLEKDWKLVTLFIGVNDLCHYCEN 980
.:KD .LVT::G NDLC.Y .:
rkksqkdpdlvtielGgNDlcdyfrd 146

SEQUENCE LISTING

SEO ID NO:1

gaageetgga acageeteet ggeeteeage aggtacagtg ageaggagte etteacegtg gttttccagc ctttcttcta tgagaccacc ccatctctac actcggagga cccccgactc caggattcta ccacgctggc ctggcatctc tggaatagga tgatggagcc agcaggagag aaagatgagc cattgagtgt aaaacacggg aggccaatga agtgtccctc tcaggagagc ccctatctgt tcagctacag aaacagcaac tacctgacca gactgcagaa accccaagac aagcttggag aaaaatccat tttccttatt tccctgtgtg tctcatttca ggtaagagaa ggageggaaa teagatgtee tgacaaagae eeeteegata eggtteeeac eteagtteat aggctgaagc cggctgacat caacgtaatt ggagccctgg gtgactctct cacggcaggc aatggggccg ggtccacacc tgggaacgtc ttggacgtct tgactcagta ccgaggcctg tcctggagcg tcggcggaga tgagaacatc ggcaccgtta ccaccctggc gaacatcctc cgggaattca accetteect gaagggette tetgttggea etgggaaaga aaccagteet aatgccttct taaaccaggc tgtggcagga ggccgagctg aggatctacc tgtccaggcc aggaggctgg tggacctgat gaagaatgac acgaggatac actttcagga agactggaag ataataaccc tgtttatagg cggcaatgac ctctgtgatt tctgcaatga tctggtccac tattctcccc agaacttcac agacaacatt ggaaaggccc tggacatcct ccatgctgag qttcctcqqq catttgtgaa cctggtgacq gtgcttgaga tcgtcaacct gagggagctg taccaggaga aaaaagtcta ctgcccaagg atgatectca ggtctctgtg tccctgtgtc ctgaagtttg atgataactc aacagaactt gctaccctca tcgaattcaa caagaagttt caggagaaga cccaccaact gattgagagt gggcgatatg acacaaggga agattttact gtggttgtgc agccgttctt tgaaaacgtg gacatgccaa agacctcgga aggattgcct gacaactett tettegetee tgactgttte caetteagea geaagtetea etceegagea gccagtgctc tctggaacaa tatgctggag cctgttggcc agaagacgac tcgtcataag tttgaaaaca agatcaatat cacatgtccg aaccagtttt tctggtccct ttcaaccctg agattctggg atttgttcta tgcccttagg ggtcatggga cctggctgcc atgcagggac agagecett etgeettgea ecetacetea gtgeatgeee tgagaeetge agacateeaa gttgtggctg ctctggggga ttctctgacc gctggcaatg gaattggctc caaaccagac gacctccccg atgtcaccac acagtatcgg ggactgtcat acagtgcagg aggggacggc

tccctggaga atgtgaccac cttacctaat atccttcggg agtttaacag aaacctcaca ggctacgccg tgggcacggg tgatgccaat gacacgaatg cattcctcaa tcaagctgtt cccggagcaa aggctgagga tcttatgagc caagtccaaa ctctgatgca gaagatgaaa gatgatcata gagtaaattt ccatgaagac tggaaggtca tcacagtgct gatcggaggc agggatttat gtgactactg cacagattcg aatctgtatt ctgcagccaa ctttgttcac catctccgca atgccttgga cgtcctgcat agagaggtgc ccagagtcct ggtcaacctc qtqqacttcc tgaaccccac tatcatgcgg caggtgttcc tgggaaaccc agacaagtgc ccagtgcagc aggccagcgt tttgtgtaac tgcgttctga ccctgcggga gaactcccaa gagetageca ggetggagge etteageega geetaeegga geageatgeg egagetggtg gggtcaggcc gctatgacac gcaggaggac ttctctgtgg tgctgcagcc cttcttccag aacatccagc teectgteet ggeggatggg eteecagata egteettett tgeeceagae tgcatccacc caaatcagaa attccactcc cagctggcca gagccctttg gaccaatatg cttgaaccac ttggaagcaa aacagagacc ctggacctga gagcagagat gcccatcacc tgtcccactc agaatgagcc cttcctgaga acccctcgga atagtaacta cacgtacccc atcaagccag ccattgagaa ctggggcagt gacttcctgt gtacagagtg gaaggcttcc aatagtgttc caacctctgt ccaccagctc cgaccagcag acatcaaagt ggtggccgcc ctgggtgact ctctgactgt gagtatggga gctcgaccaa acaactccag tgacctaccc acatcttgga ggggactctc ttggagcatt ggaggggatg ggaacttgga gactcacacc acactgeeca acattetgaa gaagtteaae eettaeetee ttggettete taecageaee tgggagggga cagcaggact aaatgtggca gcggaagggg ccagagctag ggacatgcca gcccaggcct gggacctggt agagcgaatg aaaaacagcc ccgacatcaa cctggagaaa gactggaagc tggtcacact cttcattggg gtcaacgact tgtgtcatta ctgtgagaat ccggaggccc acttggccac ggaatatgtt cagcacatcc aacaggccct ggacatcctc totgaggage teccaaggge tttegteaac gtggtggagg teatggaget ggetageetg taccagggcc aaggcgggaa atgtgccatg ctggcagctc agaacaactg cacttgcctc

SEQ ID NO:2

EAWNSLLASS RYSEQESFTV VFQPFFYETT PSLHSEDPRL QDSTTLAWHL WNRMMEPAGE

KDEPLSVKHG RPMKCPSQES PYLFSYRNSN YLTRLQKPQD KLGEKSIFLI SLCVSFQVRE

GAEIRCPDKD PSDTVPTSVH RLKPADINVI GALGDSLTAG NGAGSTPGNV LDVLTQYRGL

SWSVGGDENI GTVTTLANIL REFNPSLKGF SVGTGKETSP NAFLNQAVAG GRAEDLPVQA

RRLVDLMKND TRIHFQEDWK IITLFIGGND LCDFCNDLVH YSPQNFTDNI GKALDILHAE VPRAFVNLVT VLEIVNLREL YQEKKVYCPR MILRSLCPCV LKFDDNSTEL ATLIEFNKKF QEKTHQLIES GRYDTREDFT VVVQPFFENV DMPKTSEGLP DNSFFAPDCF HFSSKSHSRA ASALWNNMLE PVGQKTTRHK FENKINITCP NQFFWSLSTL RFWDLFYALR GHGTWLPCRD RAPSALHPTS VHALRPADIQ VVAALGDSLT AGNGIGSKPD DLPDVTTQYR GLSYSAGGDG SLENVTTLPN ILREFNRNLT GYAVGTGDAN DTNAFLNQAV PGAKAEDLMS QVQTLMQKMK DDHRVNFHED WKVITVLIGG SDLCDYCTDS NLYSAANFVH HLRNALDVLH REVPRVLVNL VDFLNPTIMR QVFLGNPDKC PVQQASVLCN CVLTLRENSQ ELARLEAFSR AYRSSMRELV GSGRYDTOED FSVVLOPFFQ NIQLPVLADG LPDTSFFAPD CIHPNQKFHS QLARALWTNM LEPLGSKTET LDLRAEMPIT CPTONEPFLR TPRNSNYTYP IKPAIENWGS DFLCTEWKAS NSVPTSVHQL RPADIKVVAA LGDSLTVSMG ARPNNSSDLP TSWRGLSWSI GGDGNLETHT TLPNILKKFN PYLLGFSTST WEGTAGLNVA AEGARARDMP AQAWDLVERM KNSPDINLEK DWKLVTLFIG VNDLCHYCEN PEAHLATEYV QHIQQALDIL SEELPRAFVN VVEVMELASL YOGOGGKCAM LAAONNCTCL RHSOSSLEKO ELKKVNWNLQ HGISSFSYWH QYTQREDFAV VVQPFFQNTL TPLNERGDTD LTFFSEDCFH FSDRGHAEMA IALWNNMLEP VGRKTTSNNF THSRAKLKCP SPESPYLYTL RNSRLLPDQA EEAPEVLYWA VPVAAGVGLV VGIIGTVVWR CRRGGRREDP PMSLRT

SEQ ID NO:3

Q05017

MALWPSVFLL GLLPLLGRGA DQIQTSSGKN TLEGQLWPES LKTFPFPCDP KTLAESVPSE
SVHSLRPSDI KFVAAIGNVE TAPDSGADDL EEQDGTEKRP EQACMGVVTV LSDIIGRFSP
SALMPLCPET RLVPRGGAED LWMQATELVR SMRENPQLDF EHDWKLINVF FSNTSQCFPC
PSAQQKGLVL GGMDKLTRTL DYLQQEVPKA FVNLVDLSEL AAFSRWRQGA QLSPAAEPCR
CLRETSQLTK VLTQWSYLEA WDSLLASSKY NTQESFAVVF QPFFYESSLS ALLAEPPLQD
PTTLALSLWN RMMEPIGRKE EPFSEKERKP LRCPTQESPY LFTYRNSGQL TRVSQPQGKL
EVREGTEIRC PDKDPSDSVP TSVHRLKPAD IKVIGAMGDS LTAGNGAGSQ PGNILDVLTQ
YRGLSWSVGG DQNISTVTTL ANILREFNPS LQGFSVGTGR ETTSQAFFNQ AVAGARADGL
IPQAQRLVAL MKNDTRINFQ EDWKIITVFI GGNDLCDFCN DPVRYSPQNF TDNIGTALDI
LHAEIPRAFV NLVKVLEISK LRELYQETKV SCPRMILRSL CPCVLKFDDN STEIASLIET
IKEYQERTQQ LIDSGRYDTR DDFTVVLQPF FEKVNMPKTQ DGLPDNSFFA PDCFHFSSKA

HAHAASALWI MMLEPVGQKT THNDFEGAVN ITCPNQVWFF LSTYKNSVQG FGTWLPCRDR SPSASPPTSV HALRPADIQV VAALGDSLTA GIGIGSKPND LSDGTTQYRG LSYSSGGDGS LDNVTTLPNI LRQFNSNLMG FAVGTGDASG TNAFFNQAVP GAKARDLMSQ VQTLVQRMKD DHRVNFQEDW KVITVQIGAS DLCDYCTDSN LYSAANFYDH LRDALDALHR EVPRALVNLV DFMNPSVTRQ VFLGNPDKCP VQQASALCNC VLSPRENSYE LARLEALAQA YQSSLRELVE SGRYDTREDF SVVLQPFFHS IQLPVLQDGR LDTSFFAPDC VHPNQKFHSQ LSRALWRNML PLGGKTDAL DLTAAITLTC PTQNEPFLRT FRNSDYTYPS RPAVENWGSD FLCTAWNASR GVPNSVHELQ PGDIKVVAAL GDSLTLAMGA RPSNSSDPPM FWRGLSWSIG GDGALETHTT LPNILKKFNP SILGFSTGTL EGTMGLNVAV QGARAQDMPA QARDLVERMF NSPEIDLEKD WKLVTLFVGG NDLCHFCENP EGSSEGEYVQ HIQQALDVLY EELPRTFVNV VEVMELAGLH QDQGGRCATL LAAQSHCTCF KYSQSSVEMQ ELKKVNWNLQ SGLSRLSYSH QYVQREDFAV VVQPFFQNTL VPLNGRGDTD LTFFSDDCFH FSERGHAEMA IALWNNMLEP VGHKTTSNNF TYSRTKLKCP SPDSPYLYTL RNSRLLPDQA EADPTVLYWA VPVAAGAGLL IGILAMVAGR GMRCRPREDP PLSLSTGL

SEQ ID NO:4
embl | AA418082 | HS1213495 . (EST)
TAAAATAGCTTTGGACTTTATTTAAATGTATCCATTCCAGGAGCATAGGCCTGGAAGAAG
CCCAGGCCCCAAGAAGTTGTGACTGTCCCCTGGGCTTCCTATGGCACCAGGCATTGAAGC
ATGTCCTGGTGGCCGGGAGTGGCTGGGGCAGAGGGCAGGGTGGCTATAGGGAG
TTTAGGGTGAGGACCCACCCCCGGGCCTAGAGGGCACCAGTGCGCAGGCTCATTGGAGGA
TCTTCCCTCCGGCCACCTCTCCTGCACCTCCAGACCACTGTCCCGATGATGCCCACCACA
AGGCCGACTCCCGCTGCCACTGGGACAGCCCAGTAGAGCACCTCGGGGGCTTCTTCAGCC
TGGTCTGGGAGCAGTCGGCTGTTCCGCAGGTTAGAGGTAAGGGCTCTCAGGAGAGGGG
CACTTGAGTTTGGCTCGGCTGTGGGTGAAGTTGTTGGAGGTAGTCTTTGCGGCCCACTGGT
TCCAGCATGTTGTTCCAGAGTGCGATGGCCATCTCGGCATGCCCGCGGTCTGAGAAGTGA
AAACAGTCCTCGGAGAAGAAGAAGGTCAGTTCCCCTTCTT

SEQ ID NO:5
genbank | AW851123 | AW851123 . (EST)
GTCCCCTGTCTTGATGGGCTGCATAGAGAGGTGCCCAGAGTCCTGGTCAACCTCGTGGAC
TTCCTGAACCCCACTATCATGCGGCAGGTGTTCCTGGGAAACCCAGACAAGTGCCCAGTG
CAGCAGGCCAGCGTTTTGTGTAACTGCGTTCTGACCCTGCGGGAGAACTCCCAAGAGCTA

GCCAGGCTGGAGGCCTTCAGCCGAGCCTACCGGAGCAGCATGCGCGAGCTGGTGGGGTCA
GGCCGCTATGACACGCAGGAGGACTTCTCTGTGGTGCTGCAGCCCTTCTTCCAGAACATC
CAGCTCCCTGTCCTGGCGGATGGGCTCCCAGATACGTCCTTCTTTGCCCCAGACTGCATC
CACCCAAATCAGAAATTCCACTCCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAA
CCACTTGGAAGCAAAACAGAGACCCTGGACCTGAGAGCAGAGATGCCCATCACCTGTCCC
ACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAAGAACTACACGTACCCCATCAAG
CCAGCCATTGAGAACTGGGGCAGTGACTTTCTGTGTACAGAAGTGGAAGCTTCCAATAGT
GGTCCAAT

SEQ ID NO:7
emb1 | A1952246 | A1952246 . (EST)
TAAAATAGCTTTGGACTTTATTTAAATGTATCCATTCCAGGAGCATAGGCCTGGAAGAAG
CCCAGGCCCCAAGAAGTTGTGACTGTCCCCTGGGCTTCCTAGGGCACCAGGCATTGAAGC
ATGTCCTGGTGGCCGGGAGTGGCTGGGCAGAGGGCGGTGAAGAGGGTGGCTATAGGGAG
TTTAGGGTGAGGACCCACCCCCGGGCCTAGAGGGCCACAGTGCGCAGGCTCATTGGAGGA
TCTTCCCTCCGGCCACCTCTCCTGCACCTCCAGACCACTGTCCCGATGATGCCCACCACA
AGGCCGACTCCCGCTGCCACTGGGACAGCCCAGTAGAGCACCTCGGGGGCTTCTTCAGCC
TGGTCTGGGAGCAGTCGGCTGTTCCGCAGGGTGTAGAGGTAAGGGCTCTCAGGAGAGGNG
CACTTGAGTTTGGCTCGGCTGTGGGT